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December 6, 2002, 23:33:11; Search time 1527.5 Seconds (without alignments) 16168.980 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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2.24.24.20 2.24.24.20 2.20.24.20 2.44.20 2.44.20 2.44.20 2.44.20 2.45.	2.68 17. 5.4 17. 1.8 17. 3.6 17. 262 17. 261 17.	00.2 20.2 20.6 20.6 20.6 20.6 20.6 20.6	99.6 200	0068 sapi 0068 0068. sapi	Homo sapiens Buckaryota; M Mammalia; Eu 1 (bases 1 1 (bases 1 2 Land; C, Yu Yu, W.; Gao, F Functional p Geduced by a Unpublished 2 (bases 1 2 (bases 1 Xu, W.; Gao, F Linstitute of Beijing 1008
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1. .2478 /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="FLB8226"

AF130068 Homo sapi AF011676 Homo sapi AK002337 Mus muscu AK004999 Mus muscu BQ643710 AGENCOURT

AF1136068 AF113676 AK002537 AK004999 BQ643710 BQ648909

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                                                                                    /note="predicted protein of HQ2209"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                  GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
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1994 AGAAGGICIGCCAGCITACATITACCCAAACIGICCATIACIGGAACCIAIGAICIGAAG 2053
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                                                                                                                                                                                                                                                                                               852 CGTCGTAGCGCTTCTCCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 911
                                                                                 792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGAT 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032 GATGAAAAGGGTACCGAGGCCGCCGCCTATGTTCCTGGAAGCTATTCCAATGAGCATT
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/note="predicted protein of HQ684"
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/product="PRO0684"
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/organism="Homo sapiens"
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/clone="FLB2803"
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/dev_stage="fetus"
/note="HQ0684"
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PTFNKITPNLAEFAFSPYRQLAHQSNSTNIFFSPYSIATAFAMISLGTKADTHDEILE
GLINFNUTEIPPRAQIHESFQELLRTLNQPDSQLQLTTGNGLFLSBGLKLVDKFLEDVKK
LYHSAFTVNFGDTEEAKKYLNNYFERFKGTYGKTVDLKKELDRTVFFANTYIFFKGKW
ERPFEVYOTEEEDFHVOYTTVWVPMMKRLGAFNIQHCKKLSSWYLLMKYLGNATAIF
FLPDGGKLQHLENELTHDIITKFLENEDRRSASLHLRKLSITGTYDLKSULGGLGITK
VFSNGADLSGYTEEAPFKLSTRAVHRAVLTIDEKGTERAGAMFLEAIPMSIPPEVKFNK
/translation="MPSSVSWGILLLAGLCCLVPVSLAEDPQGDAAQKTDTSHHDQDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 AACTTTAATTTGACCGAAATCCCAGAAGCCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG 311
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                                                                                                                                                                                                                                                                       28.0%; Score 427.4; DB 11; Length 2571; 60.1%; Pred. No. 1.7e-100;
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full.length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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2021 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG 2080
                                                                                                     2081 AGCGICCIGGGICAACIGGGCAICACIAAGGICITICAGCAAIGGGGCIGACCICICCGGG 2140
                                                                                                                                                          972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
                                                                                                                                                                                                            2141 GTCACAGAGGAGCCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATC 2200
                                                                                                                                                                                                                                                                                                   Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610011614:serine protease inhibitor 1-4, full
                                                                                                                                                                                                                                                                                                                                                                          1092 CCACCAGAAGTTAAATTAAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151
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                                                  Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:0610011614.
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                                                         /protein_id="BAB22173.1"
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Arakawa,T., Baldarelli,R., Bono,H., Bruno,M., Balt,C.,
Arakawa,T., Baldarelli,R., Bono,H., Bruno,M., Balt,C.,
Arakawa,T., Baldarelli,R., Bono,H., Brouno,M., Hanagaki,T.,
Carninoll,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,M., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Koya,S.,
Kato,H., Kawal,J., Kojlma,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Mayazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Salto,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Saski,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Takahashi,T.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshido,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liles decensions of genome exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGGGCCCGCAACTCGATTTTTTTTTTTYN 3'), CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0. Second strand CDNA was prepared with the primer adapter of sequence[5' GAGAGAGGARCCAACTCCAATTAATTAAACCCCCCCCCC 3']. CDNA was cleaved with XhoI and SStI. Cloning sites, 5' end: SStI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7.2 Suebhiro-Cho, Tsurumi-ku, Yokohama, Raitshitute; 1-7.2 Suebhiro-Cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
   Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolinga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazarelli, J., Mombaerts, P., Nordone, P., Sthopach, C., Seya, T., Shamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Stoch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weilz, C., Whittaker, C., Wilming, L., Monshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Haysshizki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/db_xref="FANTOM_DB:0610011G14"
/db_xref="MGD:MGI:1896776"
/db_xref="taxon:10090"
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COMMENT

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FSVNFAESEEAKKVINDFVEKGTOGKIVEAVKKLDOOTVFALANYILFKGKWKOPEDP
ENTEEAEFHVDESTTVKVPMYTLSGMLDVHHCSMLSSWVLLMDYAGNTAVFLLPDDG
KMOHLEOTLNKELISOFLLNRRRSDAQIHIPRLSISGNYNLKTLMSPLGITRIFNNGA
DLSGITEENAPLKLSKAVHKAVLTIDETGTEAAAATVLOVATYSMPIVRFDHPFLFI
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                                                                                                    ATULGDFALKLYRELVHQSNTSNIFFSFVSITATFAMLSLGSKGDTHTQILEGLQFNL
TQTSEADIHKSFQHLLQTLNRPDSELQLSTGNGLFVNNDLKLVEKFLEEAKNHYQAEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 GGGAACCCAAGGAAAGATAGTTGAGGCGGTGAAAAACTGGACCAAGACACACAGTTTTCGC 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 ITTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTT 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 TCAAAGTAATTCTACTAACATTTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 TCTGGCTGAGGATGTTCAGGAGACAGACACCTCCCAGAAGGATCAGTCC---CCAGCCTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 CCATGAGATCGCTACAAACCTGGGAGACTTTGCCCTCAGACTATACAGGGAGCTGGTCCA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.7%; Score 331.2; DB 11; Length 1392; 56.3%; Pred. No. 1.9e-75;
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishina,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Kokazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 2053013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
                                                                                                      970 TGCTCAGATCCATATCCCCAGACTGTCCTCTGGAAACTATAACTTGAAGACACTCAT 1029
                                                                                                                                                                              980 AG---AAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGA 1036
                                                                                                                                                                                                                                                                1037 AAAGGTACCGAGGCCGCCGCGCGTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACC 1096
                                                                                                                                                                                                                                                                                                                                                 1097 AGAAGTTAAATTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAAAGCCC 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1210 TATCGTGCGCTTCGACCACCCTTTCCTTTTCATAATATTTGAAGAACACACTCAGAGCCC 1269
910 GGAGCAAACTCTCAACAAGGAGCTCATCTCTCAGTTCCTGCTAAACAGGGGAGAAGCGA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300014A17:serine protease inhibitor 1-4, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone_lib_RIKEN_full-length enriched mouse cDNA library
                                                             860 CGCTTCTCCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTT
                                                                                                                                                   920 AGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
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Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Balaloy, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stabili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolinga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Garibold, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection by Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachl, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishli, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramcto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kurihara, C., Matsuyama, T., Miyazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, Y., Shinagawa, A., Sasaki, D., Sogabo, Y., Suzuki, H., Tagami, W., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1296
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
RAREN Yokohama (1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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/organism="Mus musculus"
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ENTKOAEFHVDESTTYKVPMATLSGMLDVHGCSTLSSWVLLMDYAGRATAVFLLPDDG
KMCHEQUTNKELISKFLLINRRRLAQIHIPRLSISGNYNLETLMSPLGITRIFNSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 GTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAAACTTTAA 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 GAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCTGAAGG 379
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                        /note="data source:MGD, source key:MGI:891968,
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Pred. No. 4.1e-72;
0; Mismatches 516; Indels
                                                                                                   serine protease inhibitor 1-4"
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/qene="Spil-4"
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55.6%;
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/note="Organ: liver: Vector: pOTB7; Site_1: Xho1; Site_2: ECORI; CDNA made by oligo-dr priming. Directionally cloned into ECORI/Xho1 sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
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AGENCOURT_8342217 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6268225
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                         950 AGCCCAGATCCATATCCCCAGACTGTCCATCTTGGAAACTATAACTTGGAGACACTCAT 1009
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                                                 800 AGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAG 859
830 TIACGCGGGCAACGCCACTGCTCTTCCTCCTGCCCGATGATGGGAAGATGCAGCATCT 889
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Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nih.90v

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llh.gov
Plate: LLCM2439 row: n column: 02
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                920 AGGCCAGTTAGGTATTACCAAAGTTTTTTTTTAACGGTGCCGATTTGAGTGGTGTTACTGA
                                                                                                                                                                                                                                                                                                1070 GGAGAAIGCICCCCIGAAGCICAGCCAGGCIGIGCATAAAGGCCGIGCIGACCAICGAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1037 AAAGGGTACCGAGGCCGCCGGCGCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1130 GACAGGAACAGAAGCTGCAGCAGCTACAGTCTTACAAGGCGGTTTTTTGTCTATGCCCCC
                                                                                                       890 GGAGCAAACTCTCAACAAGGAGCTCATCTTAAGTTCCTGCTAAACAGGCGCAGAAGGTT
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Location/Qualifiers
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using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                    375 GAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAG 434
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                                                                            20.3%; Score 309.8; DB 14; Length 887; 60.0%; Pred. No. 6.5e-70;
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8Q648909 907 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8351269 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6286839
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capabs-refmail.nih.gov
Enail: capabs-refmail.nih.gov
CONA Library Preparation: Rubin Laboratory
CONA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://image.lih.gov
Plate: LLCM2488 row: e column: 16
High quality sequence stop: 721.
                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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895 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8349591 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284550
BQ653587
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/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                              IICAACAIIGCAAAAAIIAAGIICIIGGGICIIAIIAAIGAAGIAIIIAGGIAACGCIA 756
                                      375 TCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCC 434
                                                                                                    TTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGAAGATTTTC
                                                                               637 ATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAGACTGGGTATGTTCAATA
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BQ653587
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ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II. RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 6.6e-64;
0; Mismatches 317; Indels
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Best Local Similarity 60.1%;
Matches 477; Conservative
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RESULT

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AGENCOURT_8492569 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6296341
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Contact: Robert Strausberg, Ph.D.
Email: gapba-remail.nin.gov
Tissue Procurement: Cape (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lange.llnl.gov
Plate: LLCM2604 row: a column: 14
High quality sequence stop: 647.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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985 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6709923 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760183 BM924019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 985)
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663 GTTCCAATGATGAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAATTAAGTTCT 722
                         661 CCTCTCCGGGGTCACAGAGGAAGCACCCTGAAGCTCTCCAAGGCGGTGCATAAGGCTGT 720
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2806 row: m column: 16
High quality Sequence stop: 707.
                                                                                                                                                                                                                                                             843 AACGAGGATCGTCGTAGCGCTTCTCGCACCTGCCAAAGTTAAGTATCACCGGTACTTAC 902
                                                                                                                                                                                                                                                                                                      541 AATGAAGACAGAGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTAT 600
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National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   962 ITTGAGTGGTGTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_116"
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/note="Organ: prostate; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; CDNA made by oligo-dT priming.

Site_2: ECORI; CDNA made by oligo-dT priming.

Directionally cloned into ECORI/ANDI Sites using the following 5' adaptor: GGCACGGG(): Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit (Stratagene) and Superscript II TT (Life Technologies).

Note: this is a NH_MGC Library."
AGENCOURT_10034701 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483305
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 AAATIGGIIGACAAAIICCIAGAAGACGICAAGAAACIAIAICAIAGIGAGGCIITIACC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 GTTAATTTTGGTGATACTGAGGAAGCTAAAAGCAAATTAATGATTATGTTGAGAAAGGC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AGTITAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAAACTTTAAATTTG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 ACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTGAGAACTTTGAAT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAAC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CAACCIGAIICICAAIIGCAAIIAACIACIGGIAACGGIIIAIIIIITGICIGAAGGIIIA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGCCCTGAATTTCAACCTC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AAAATTACTCCAAATTTAGCCGAATTTGCTTTTTTTTTGTATAGACAATTAGCTCATCAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 AGTAATTCTACTAACATTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCATGTTG 203
                                                                                                                                                                                                                                                                          NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 283.8; DB 14; Length 924;
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0; Mismatches 363; Indels
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/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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High quality sequence stop: 586.
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                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6483305"
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                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                      BQ958958.1 GI:22374436
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BQ958958
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                                         destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 CIGGCACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCC 271
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                                                                                                                                                                                                                                                                                                                                                                                                                  92 GAGGATCCCCAGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 CCAACCTICAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG 211
                                                                                                                                                                                                                                                                                                                    2; Gaps
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AGENCOURT_8298326 NIH_MGC_100 Homo saplens cDNA clone IMAGE:6269613 BQ650189
      stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site i destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCCGCCGCCGCCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACCAGAAGTTAAAT 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTATATTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGG 627
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                                                                                                                                                                                                                                                                                          448 ATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCC 507
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                                                                                                                                                                                                            DB 14; Length 1194;
                                                                                                                                                                                                        18.0%; Score 274.8; DB 14; Length 61.2%; Pred. No. 9.7e-61;
tive 0; Mismatches 282; Indels
                                                                                                                                                                                                                                                    Matches 444; Conservative
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of 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1194)
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                                     504 ACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTA 563
                                                                           ACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGGTTTTTGCTCTG 481
                                                                                                                       GTTAACTATATTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAA 623
                                                                                                                                         GAGGAAGATITICATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAGACTG 683
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12809 row: J column: 20
                                                                                                                                                                                                                           GTCAACTTCGGGGACACCGAAGAGGCCAAGAACAGATCAACGATTACGTGGAGAAGGGT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                        AATGAGTTGACTCATGACATTATTACTAAATT - - TTTAGAGAACGAGGATCGTCGTAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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High quality sequence stop: 662.
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_116"
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/clone='InAGE:5269013"
/clone=Lib="NIH_MGC_100"
/tissue_type='hepatocellular carcinoma, cell line"
/tissue_type='hepatocellular carcinoma, cell line"
/tab_host="bild (hage-resistant)"
/note="organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
/note: congruent of the following 5' adaptor:
/note Scori/Aho Site_selected >500bp for average insert size
/note Scori/Aho (university of California, Berkeley)
/note Stories Stori
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                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs rémail.nih.gov
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Conne distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov
Plate: LLCM2443 row: g column: 22

High quality sequence stop: 650.
                                                                                                                   Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   1 (bases 1 to 907)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="hepatocellular carcinoma, cell line"
/lab_host="bH10B (phage-resistant)"
/note="Organ: liver: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dī priming. Directionally cloned
into ECORIXADI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I. 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                             427 ACCGCCATCTTCCTGCCTGATGAGGGGAACTACAGCACTGGAAAATGAACTCACC 486
                                                                                                                             816 CAIGACAITAITACTAAATITITAGAGAACGAGGAICGTCGTAGCGCITCTCTGCACCIG 875
                                                                                                                                                                            936 ACCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAAAA 995
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876 CCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGCCAGTTAGGTATT
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Tissue Procurement: CGAP (Stanford)
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/clone="IMAGE:6269919"
/clone_lib="NIH_MGC_100"
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AGENCOURT_8302495 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271313
5', mRNA sequence.
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                                                                                                      1 ACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAG 60
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                                   Score 270.4; DB 14; Length 959;
Pred. No. 1.3e-59;
0; Mismatches 326; Indels 1;
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                                   17.7%;
59.3%;
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                                                        Matches 477; Conservative
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/organism="Homo sapiens"
/db_ref="taxon:9606"
/clone="INAGE:6271313"
/clone_lib="NIH_MGC_l00"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_hog="repair" ilver; vector: pormar); Site_l: XhoI; Site_2:
/note="Organ: liver; vector: priming. Directionally cloned
into EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI; Abol sites using the following 5' adaptor:
GGCAGGAG(G). Size=selected >500bp for average insert size
I. Rb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of Callifornia, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT. (Life Technologies). Note: this is a NIH_MGC
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Gape (Stanford)
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2447 row: n column: 18
High quality sequence stop: 672.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 AATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AACTITAAITITGACCGAAAICCCAGAAGCCCAAAITCACGAGGGITITCAAGAGITGTIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTG
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Pred. No. 3.7e-59;
0; Mismatches 314; Indels 2;
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Similarity 60.3%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                          602589741F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723498 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue procurement: CLONGIECH Laboratories, Inc.

CDNA Library Preparation: CLONGIECH Laboratories, Inc.

CDNA Library Preparation: CLONGIECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI583 row: b column: 11

High quality sequence stop: 730.
                                                                            747
                                                                                                                                                                                       GATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAAATTAAGTTCTTGGGTCTT 730
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                           GTCTTCGCACTAGTTAACTATATTTTTTTAAGGGTAAGGGAACGTCCTTTCGAGGTT
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GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC
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                                                        55 ATCACGACCAAGACCATCCGACTTTTAATAAATTACTCCAAATTTAGCCGAATTTGCTT 114
                                                                                                                ITICIATIGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACG 234
                                                                                                                                                                                                                                                                                       295 GITITICAAGAGITGITGAGAACTITGAATCAACCTGAITCTCAATTGCAATTAACTACTG 354
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Pred. No. 5.1e-59;
0; Mismatches 317;
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